



1652

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/644,668A

DATE: 04/29/2002
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3 <110> APPLICANT: Korman, Alan J.
4 Halk, Edward L.
5 Lonberg, Nils
6 Medarex, Inc.
8 <120> TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
10 <130> FILE REFERENCE: 014643-010510US
12 <140> CURRENT APPLICATION NUMBER: US 09/644,668A
13 <141> CURRENT FILING DATE: 2000-08-24
15 <150> PRIOR APPLICATION NUMBER: US 60/150,452
16 <151> PRIOR FILING DATE: 1999-08-24
18 <160> NUMBER OF SEQ ID NOS: 41
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3159
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence:cloning vector
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34 aaagccccgtt cattaggcgg gctcttggca gaacatatcc atcgcgtccg ccatctccag 180
35 cagccgcacg cggcgcatct cgggcagcgt tgggtcctgg ccacgggtgc gcatgatcgt 240
36 gctcctgtcg ttgaggaccc ggctaggctg gcggggttgc cttactgggtt agcagaatga 300
37 atcaccgata cgcgagcga cgtgaagcga ctgctgctgc aaaacgtctg cgacacctgagc 360
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39 gcccctgcacc attatgttcc ggatctgcat cgcaggatgc tgctggctac cctgtggAAC 480
40 acctacatct gtattaaacga agcgctggca ttgaccctga gtgatttttc tctggtccc 540
41 cgcgcattccat accgcccagt ttatcaccctc acaacgttcc agtaaccggg catgttcatc 600
42 atcagtaacc cgtatcgta gcatcctctc tcgttccatc ggtatcatc ccccatgaa 660
43 cagaaattcc cccttacacg gaggcatcaa gtgaccaaagc agaaaaaaac cgcgcattaa 720
44 atggccccgtt ttatcagaag ccagacatta acgcttctgg agaaactcaa cgagctggac 780
45 gcgatgaac aggcagacat ctgtgaatcg cttcacgacc acgctgtatga gcttaccgc 840
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47 acggtcacag ctgtctgtc agcggtgcc gggagcagac aagccgtca gggcgctca 960
48 gcgggtgttg gcgggtgtcg gggcgccagcc atgaccctgt cactgtatcg tagcgagtg 1020
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50 gtgaaatacc gcacagatgc gtaaggagaa aataccgcatt caggcgctt tccgttcc 1140
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 56 cgaccctgcc gcttaccgga tacctgtccg cctttctccc ttcggaaagc gtggcgctt 1500
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 60 aagaggccac tggtaacagg attagcagag cgaggtatgt aggcgggtgt acagagttct 1740
 61 tgaagtgggt gcctaaactac ggctacacta gaaggacagt atttggtatac tgcgtctgc 1800
 62 tgaaggccagt taccttcgga aaaagagttt gtagctttt atccggcaaa caaaccaccc 1860
 63 ctggtagcgg tggttttttt gtttgcaggc agcagattac ggcgcagaaaa aaaggatctc 1920
 64 aagaagatcc ttgtatctt tctacggggt ctgacgctca gtggaaacgaa aactcacgtt 1980
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 66 aatgaagttt taaatcaatc taaagtatata atgagtaaac ttggctctgac agttaccaat 2100
 67 gcttaatcag tgaggcacct atctcagcga tctgtctatt tcgttcatcc atagttgcct 2160
 68 gactccccgt cgttagata actacgatac gggagggtt accatctgc cccagtgc 2220
 69 caatgataacc gcgagaccca cgctcaccgg ctccagattt atcagcaata aaccagccag 2280
 70 ccggaaaggc cgagcgcaga agtggctctg caactttatc cgcctccatc cagtttatttt 2340
 71 attttttccg ggaagctaga gtaagtagtt cgccagttaa tagtttgcgc aacgttgg 2400
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 78 gaaaacgttc ttccggccgaa aaactctcaa ggatcttacc gctgttgaga tccagttcga 2820
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 81 gttgaataact catacttttc cttttcaat attattgaag catttatcag gtttattgtc 3000
 82 tcatgagcgg atacatattt gaatgtattt agaaaaataa acaaataagg gttccgcga 3060
 83 cattttcccg aaaagtccca cctgacgtct aagaaccat tattatcatg acattaacct 3120
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88 <211> LENGTH: 349

89 <212> TYPE: DNA

90 <213> ORGANISM: Homo sapiens

92 <220> FEATURE:

93 <223> OTHER INFORMATION: preliminary sequence for heavy chain fragment
94 10D1.3

96 <400> SEQUENCE: 2

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98 cacccatgtt agctataacta tgcactgggtt ccggccaggctt ccaggcaagg ggctggatgt 120

99 ggtgacattt atatcatatg atggaaacaa taaatactac gcagactccg tgaaggccg 180

100 attcaccatc tccagagaca attccaagaa cacgtgtat ctgcaaatac acagcctgag 240

101 agctgaggac acggcttatattactgtc gaggaccggc tggctgggc cctttgacta 300

102 ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc accaaggc 349

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106 <211> LENGTH: 321

107 <212> TYPE: DNA

108 <213> ORGANISM: Homo sapiens

110 <220> FEATURE:

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 116 agagtgttgg cagcagctac ttagcctgtt accagcagaa acctggccag gctcccaggc 120
 117 tcctcatcta tggtgcatcc agcagggcca ctggcatccc agacaggttc agtggcagtg 180
 118 ggtctgggac agacttcaact ctcaccatca gcagactgga gcctgaagat tttgcagtgt 240
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 120 tcaaacgaac tgtggctgca c 321
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 124 <211> LENGTH: 287
 125 <212> TYPE: DNA
 126 <213> ORGANISM: Homo sapiens
 128 <220> FEATURE:
 129 <223> OTHER INFORMATION: Vk A-27 germline sequence
 131 <400> SEQUENCE: 4
 132 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 133 ctctcctgc gggccagtca gagtgttagc agcagctact tagcctgta ccagcagaaaa 120
 134 cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180
 135 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 136 cctgaagatt ttgcagtgtta ttactgtcag cagtatggta gctcacc 287
 139 <210> SEQ ID NO: 5
 140 <211> LENGTH: 95
 141 <212> TYPE: PRT
 142 <213> ORGANISM: Homo sapiens
 144 <220> FEATURE:
 145 <223> OTHER INFORMATION: light chain variable region predicted sequence for
 146 Vk A-27 germline
 148 <400> SEQUENCE: 5
 149 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 150 1 5 10 15
 152 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 153 20 25 30
 155 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 156 35 40 45
 158 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 159 50 55 60
 161 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 162 65 70 75 80
 164 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser
 165 85 90 95
 168 <210> SEQ ID NO: 6
 169 <211> LENGTH: 325
 170 <212> TYPE: DNA
 171 <213> ORGANISM: Homo sapiens
 173 <220> FEATURE:
 174 <223> OTHER INFORMATION: light chain variable region (V_k), 10D1 from V_k
 175 A-27
 177 <400> SEQUENCE: 6

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 179 ctctcctgca gggccagtca gagtggttgc agcagctact tagcctggta ccagcagaaa 120
 180 cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180
 181 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 182 cctgaagatt ttgcagtgtta ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300
 183 caagggacca aggtgaaat caaac 325

186 <210> SEQ ID NO: 7
 187 <211> LENGTH: 108
 188 <212> TYPE: PRT
 189 <213> ORGANISM: Homo sapiens
 191 <220> FEATURE:
 192 <223> OTHER INFORMATION: light chain variagle region predicted sequence for
 193 10D1 from Vk A-27

195 <400> SEQUENCE: 7

196 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 197 1 5 10 15

199 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
 200 20 25 30

202 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 203 35 40 45

205 Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 206 50 55 60

208 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 209 65 70 75 80

211 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 212 85 90 95

214 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 215 100 105

218 <210> SEQ ID NO: 8
 219 <211> LENGTH: 325
 220 <212> TYPE: DNA
 221 <213> ORGANISM: Homo sapiens
 223 <220> FEATURE:
 224 <223> OTHER INFORMATION: light chain variable region (Vk) 4B6 from Vk A-27
 226 <400> SEQUENCE: 8

227 gaaattgtgt tgacgcagtc tccaggcacc ctgtcttgc ctccagggga aagagccacc 60
 228 ctctcctgca gggccagtca gagtggttgc agcagttct tagcctggta ccagcagaaa 120
 229 cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180
 230 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 231 cctgaagatt ttgcagtgtta ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300
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235 <210> SEQ ID NO: 9
 236 <211> LENGTH: 108
 237 <212> TYPE: PRT
 238 <213> ORGANISM: Homo sapiens
 240 <220> FEATURE:
 241 <223> OTHER INFORMATION: light chain variable region predicted sequence for
 242 4B6 from Vk A-27
 244 <400> SEQUENCE: 9

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245 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
246 1 5 10 15
248 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
249 20 25 30
251 Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
252 35 40 45
254 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
255 50 55 60
257 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
258 65 70 75 80
260 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
261 85 90 95
263 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
264 100 105
267 <210> SEQ ID NO: 10
268 <211> LENGTH: 287
269 <212> TYPE: DNA
270 <213> ORGANISM: Homo sapiens
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Vk L-15 germline sequence
275 <400> SEQUENCE: 10
276 gacatccaga tgaccaggc tccatcctca ctgtctgcat ctgttaggaga cagagtcacc 60
277 atcaacttgc gggcgagtca gggattttagc agctggtag cctggtatca gcagaaacca 120
278 gagaaaagccc ctaagtccct gatctatgt gcatccagtt tgcaaagtgg ggtcccatca 180
279 aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
280 gaagatttttcaacttattatcgtccaaacag tataatagtt accctcc 287
283 <210> SEQ ID NO: 11
284 <211> LENGTH: 94
285 <212> TYPE: PRT
286 <213> ORGANISM: Homo sapiens
288 <220> FEATURE:
289 <223> OTHER INFORMATION: light chain variable region predicted sequence for
290 Vk L-15 germline
292 <400> SEQUENCE: 11
293 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
294 1 5 10 15
296 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
297 20 25 30
299 Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
300 35 40 45
302 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
303 50 55 60
305 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
306 65 70 75 80
308 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr
309 85 90
312 <210> SEQ ID NO: 12
313 <211> LENGTH: 322
314 <212> TYPE: DNA

VERIFICATION SUMMARY

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